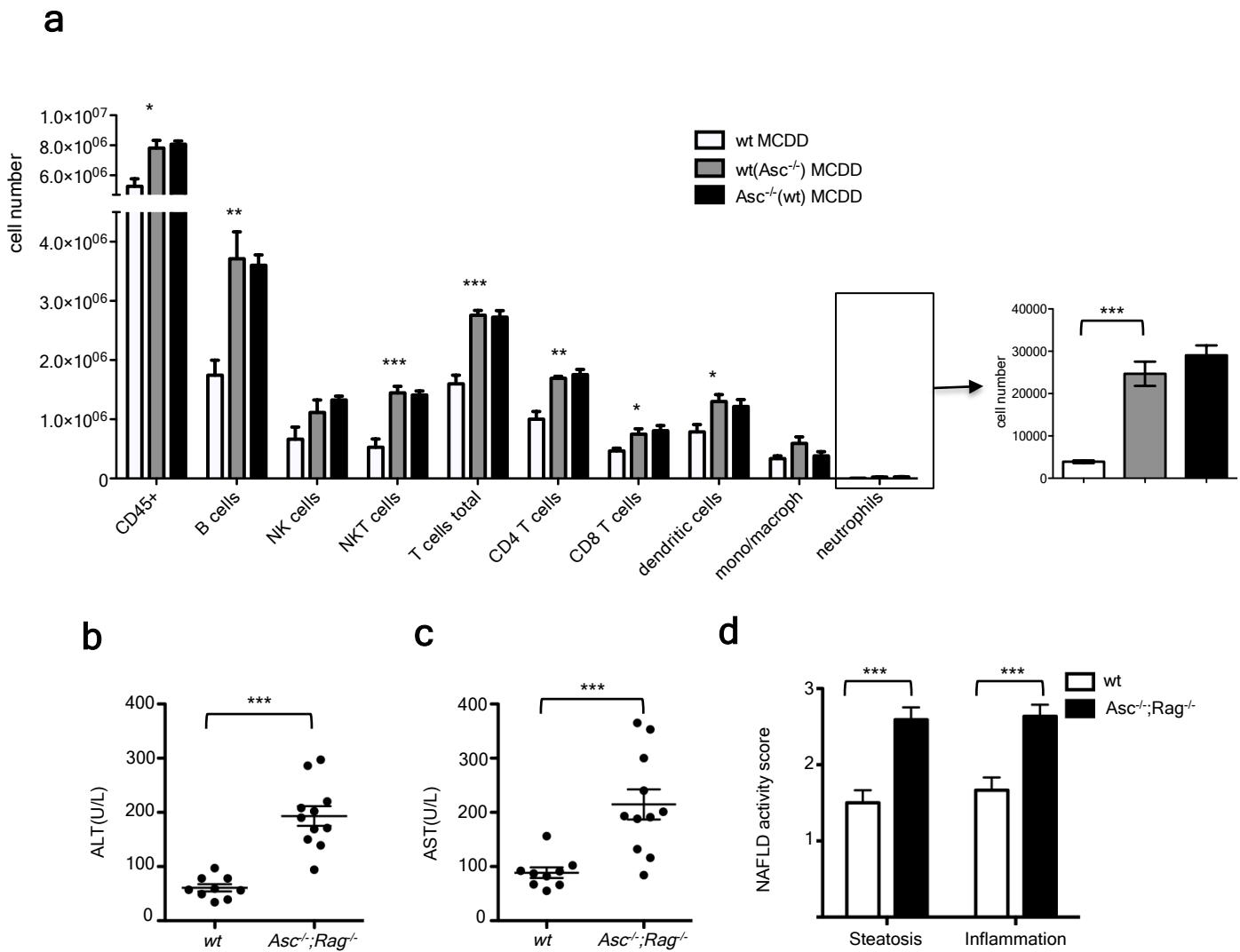
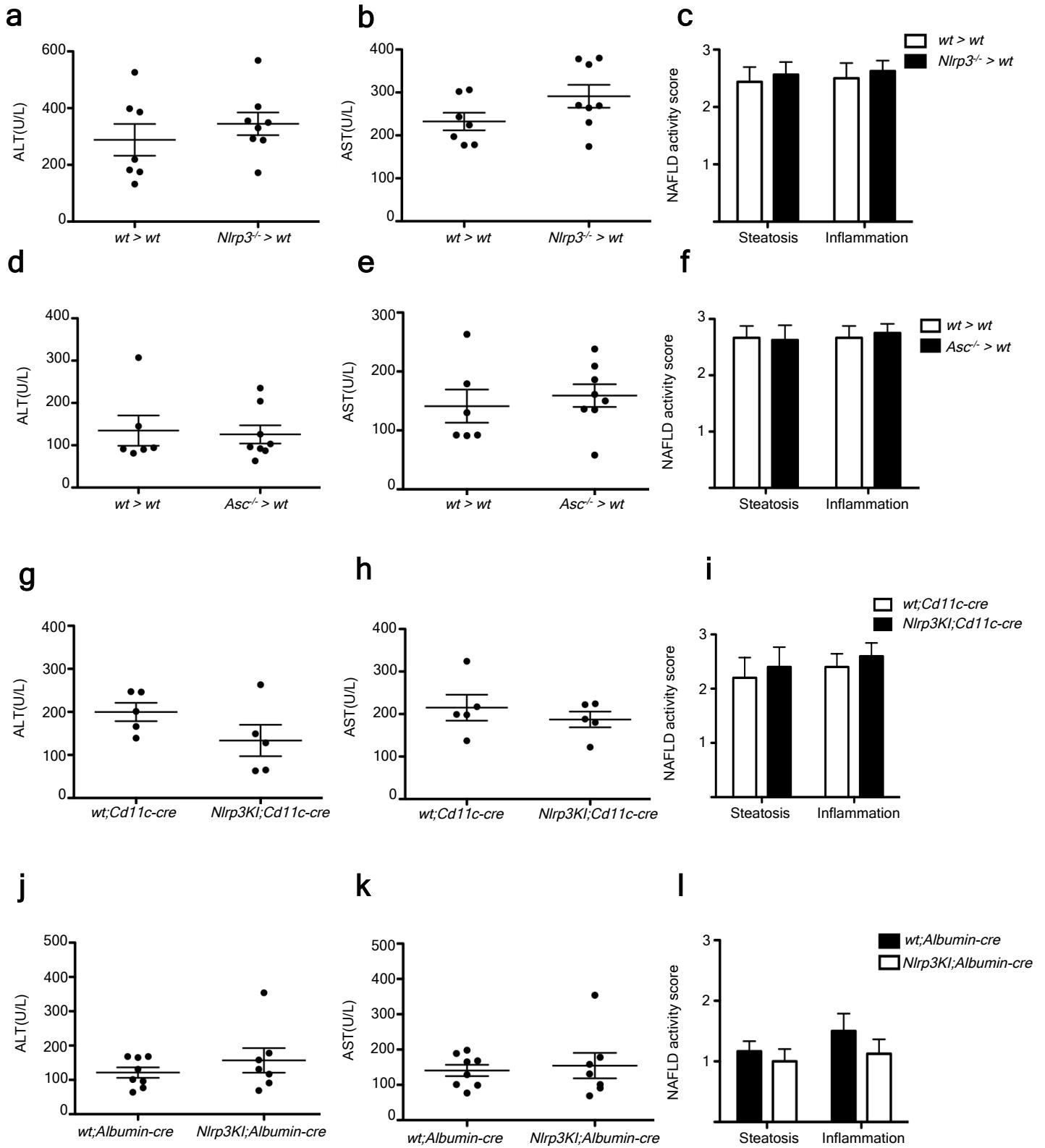


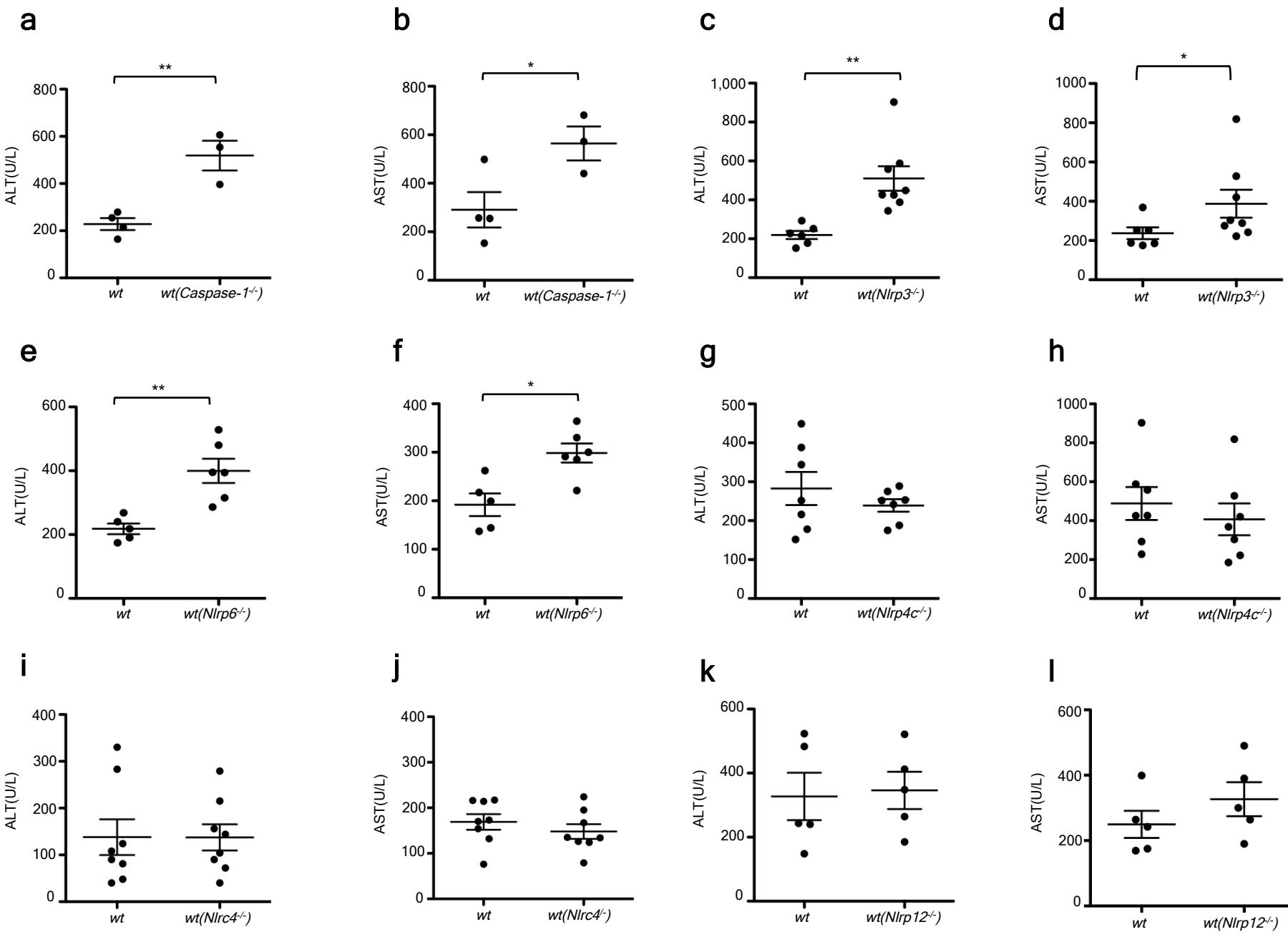
Supplemental figure 1. Increased severity of NASH in inflammasome-deficient mice, but not in II1r-deficient animals. To induce NASH, mice were fed with MCDD for 24 d. Their serum ALT and AST activities measured and NAFLD histological activity scores were determined. (a-b) Comparison of ALT, AST, and NAFLD activity, plus histological scores for steatosis and inflammation between singly-housed wild-type (*wt*) mice and *II1r^{-/-}* animals. (c) Representative hematoxylin and eosin (H&E)-stained sections of livers from *wt*, *Caspase-1^{-/-}*, *Asc^{-/-}*, *Nlrp3^{-/-}*, *II18^{-/-}*, and *II1r^{-/-}* mice. Inflammatory foci are highlighted with an arrowhead. Data represent two independent experiments (n=7-19 mice/treatment group). Error bars represent the SEM of samples within a group. Scale bars = 200 μ m (K). *p \leq 0.05, **p \leq 0.01, ***p \leq 0.001 (Student's t test).



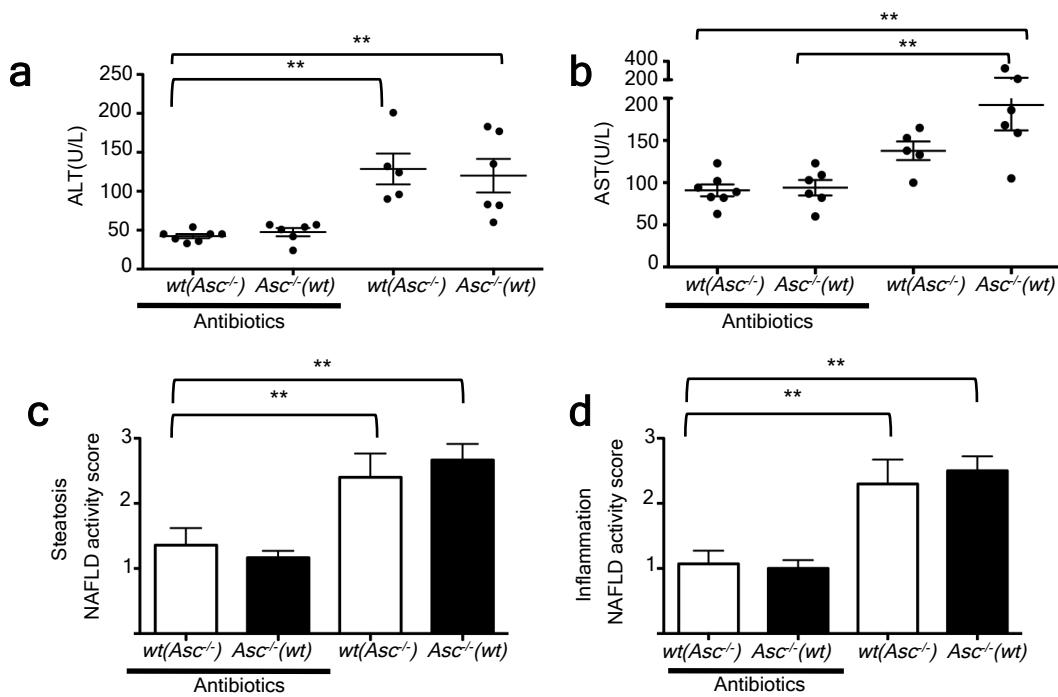
Supplemental figure 2. Changes in liver cellularity in MCDD-fed *Asc*-deficient mice and cohoused *wt* animals. Singly-housed *wt*, co-housed *Asc*^{-/-} (*wt*), and co-housed *wt*(*Asc*^{-/-}) animals were fed MCDD for 24 d to induce NASH, and hematopoietic cell subsets in liver were quantified by FACS. (a) Total numbers of CD45⁺ cells, B cells (B220⁺), T cells (TCR β ⁺), CD4+ T cells, CD8+ T cells, NK cells (NK1.1⁺ TCR β ⁺), NKT cells (NK1.1⁺ TCR β ⁺), dendritic cells (CD11c⁺ CD11b⁺), mononuclear macrophages (MHCII⁺ CD11b⁺), and neutrophils (Gr1⁺). *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001 between the *wt* single housed group and the co-housed *wt*(*Asc*^{-/-}) animals (Student's t test). Data is representative of two independent experiments. (b-d) Comparison of serum ALT, serum AST, plus NAFLD activity histological scores for steatosis and inflammation in *wt* and compound homozygous knockout *Asc*^{-/-};Rag^{-/-} mice. Error bars represent the SEM of samples within a group. *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001 (Student's t test).



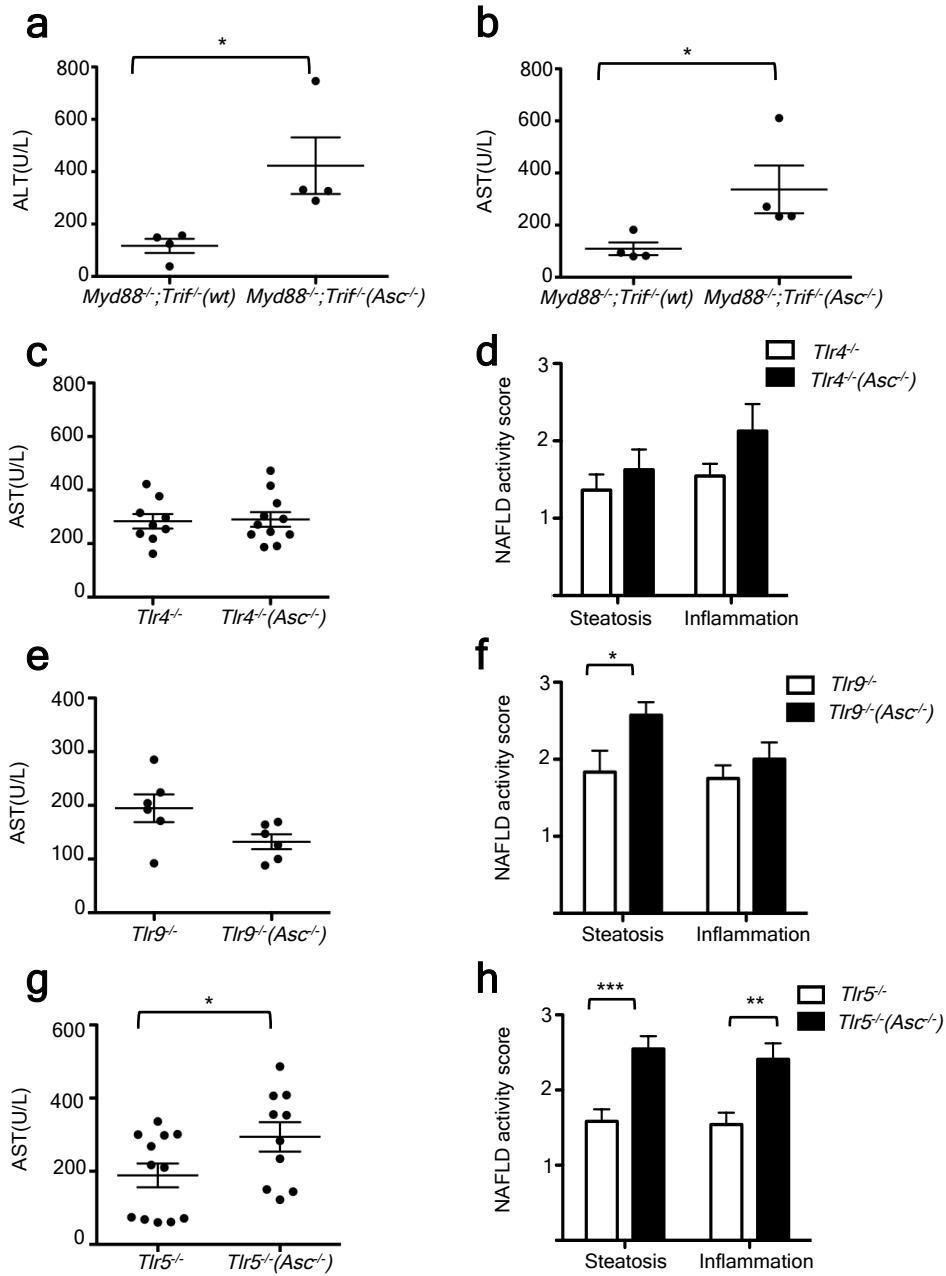
Supplemental figure 3. Activation of the NLRP3 inflammasome in hematopoietic cells and hepatocytes does not influence NASH severity. To induce NASH, mice were given MCDD for 24 d, and their serum ALT and AST activities, and NAFLD histological activity scores were determined. (a-f) Comparison of ALT, AST, and NAFLD activity histological scores for steatosis and inflammation between chimeric mice generated with *wt* (*wt* > *wt*) and *Nlrp3*^{-/-} (*Nlrp3*^{-/-} > *wt*) bone marrow (BM) (a-c) or *Asc*^{-/-} (*Asc*^{-/-} > *wt*) BM (d-f). (g-l) Comparison of serum ALT and AST activities, and NAFLD activity histological scores for steatosis and inflammation between *wt;CD11c-Cre* and *Nlrp3Kl;CD11c-Cre* mice (g-i) or *wt;Albumin-Cre* and *Nlrp3Kl;Albumin-Cre* mice (j-l). Error bars represent the SEM of samples within a group. *p≤0.05, **p≤0.01, ***p≤0.001. (Student's t test)



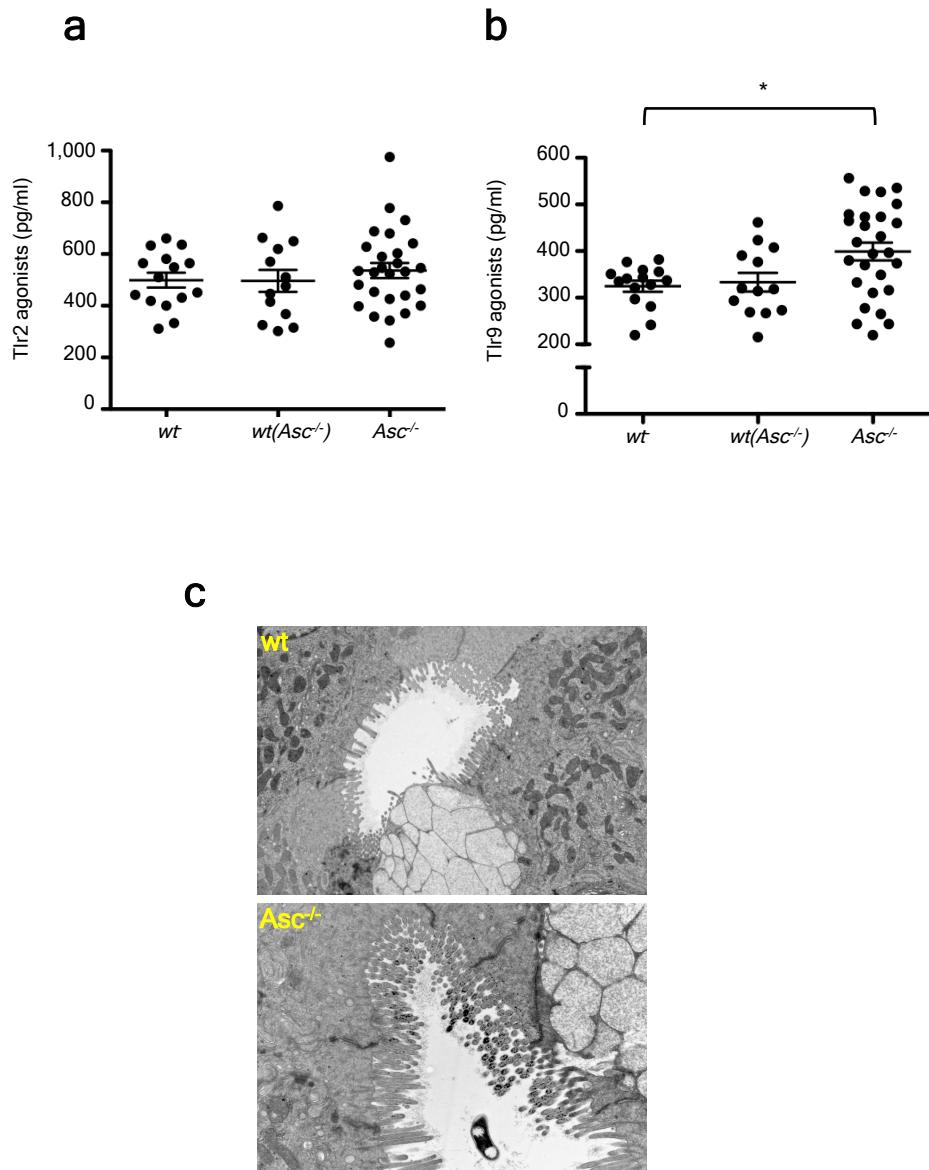
Supplemental figure 4. Increased severity of NASH in caspase-1-, Nlrp3-, and Nlrp6-deficient mice is transmissible to co-housed wild-type animals. Singly-housed wt (wt) mice and wt mice co-housed with caspase-1^{-/-} animals (wt (caspase-1^{-/-})) (a,b), Nlrp3^{-/-} animals (wt(Nlrp3^{-/-})) (c,d), Nlrp6^{-/-} animals (wt(Nlrp6^{-/-})) (e,f), Nlrp4c^{-/-} mice (wt(Nlrp4c^{-/-})) (g,h), Nlrc4^{-/-} mice (wt(Nlrc4^{-/-})) (i,j), and Nlrp12^{-/-} mice (wt(Nlrp12^{-/-})) (k,l) were given MCDD for 24 d to induce NASH. Comparison of serum ALT and AST activities in wt and wt(caspase-1^{-/-}) (a,b), wt(Nlrp3^{-/-}) (c,d), wt(Nlrp6^{-/-}) (e,f), wt(Nlrp4c^{-/-}) (g,h), wt(Nlrc4^{-/-}) (i,j), and (wt(Nlrp12^{-/-})) (k,l) animals. Error bars represent the SEM of samples within a group (n=3-8 mice/group). *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001. (Student's t test)



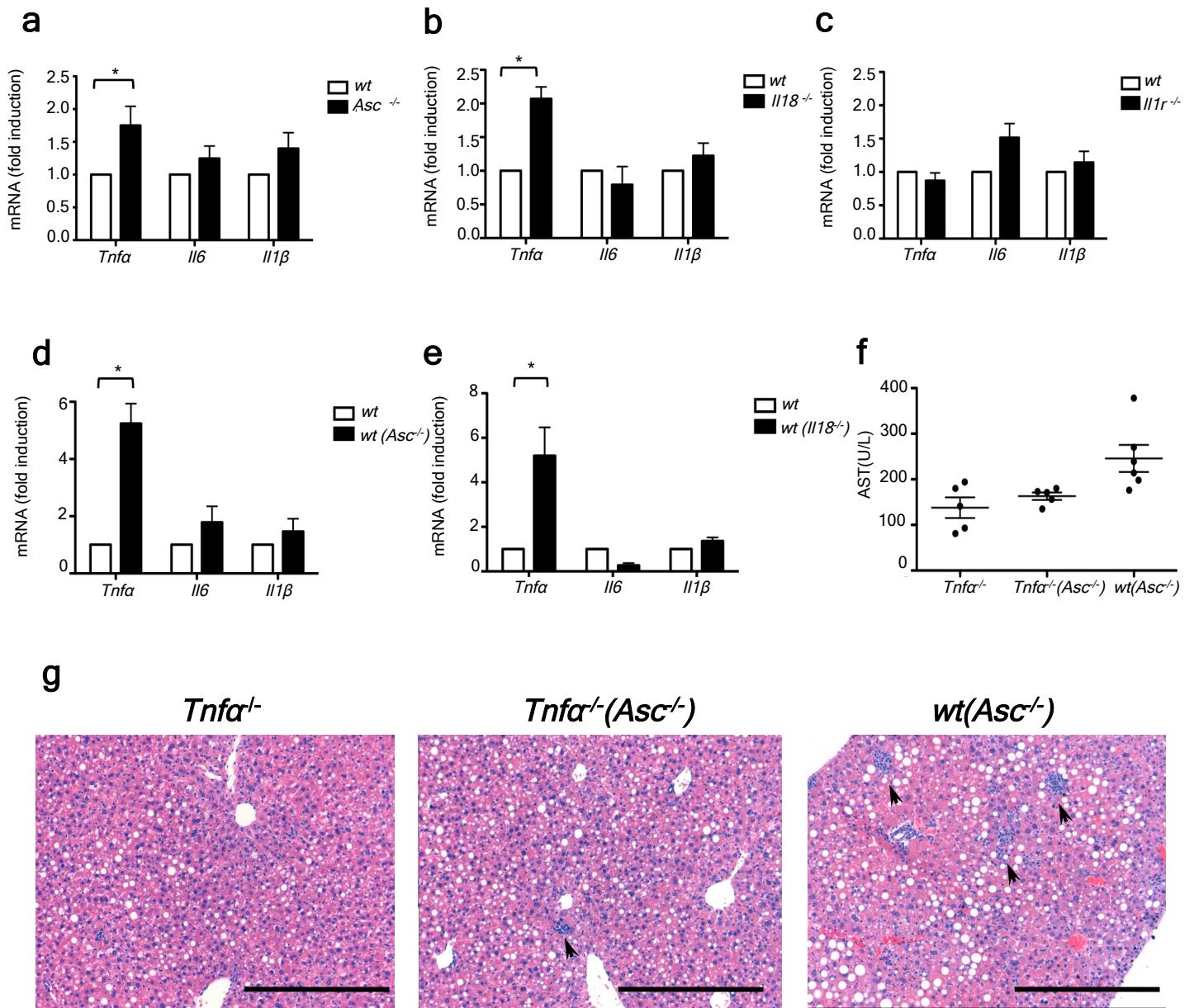
Supplemental figure 5. The increased severity of NASH in *Asc* and *Il18*-deficient mice and co-housed wild-type animals is abolished with antibiotic treatment. (a-d) Comparison of serum ALT (a) and AST (b), plus NAFLD activity histological scores for steatosis (c) and inflammation (d) of *wt (Asc^{-/-})* and *Asc^{-/-}(wt)* mice that were untreated or treated orally with a combination of metronidazole and ciprofloxacin for 4 weeks. Inflammatory foci are highlighted with an arrowhead. Data are represents two independent experiments (n=5-7 mice/treatment group). Error bars represent the SEM of samples within a group. *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001. (ANOVA)



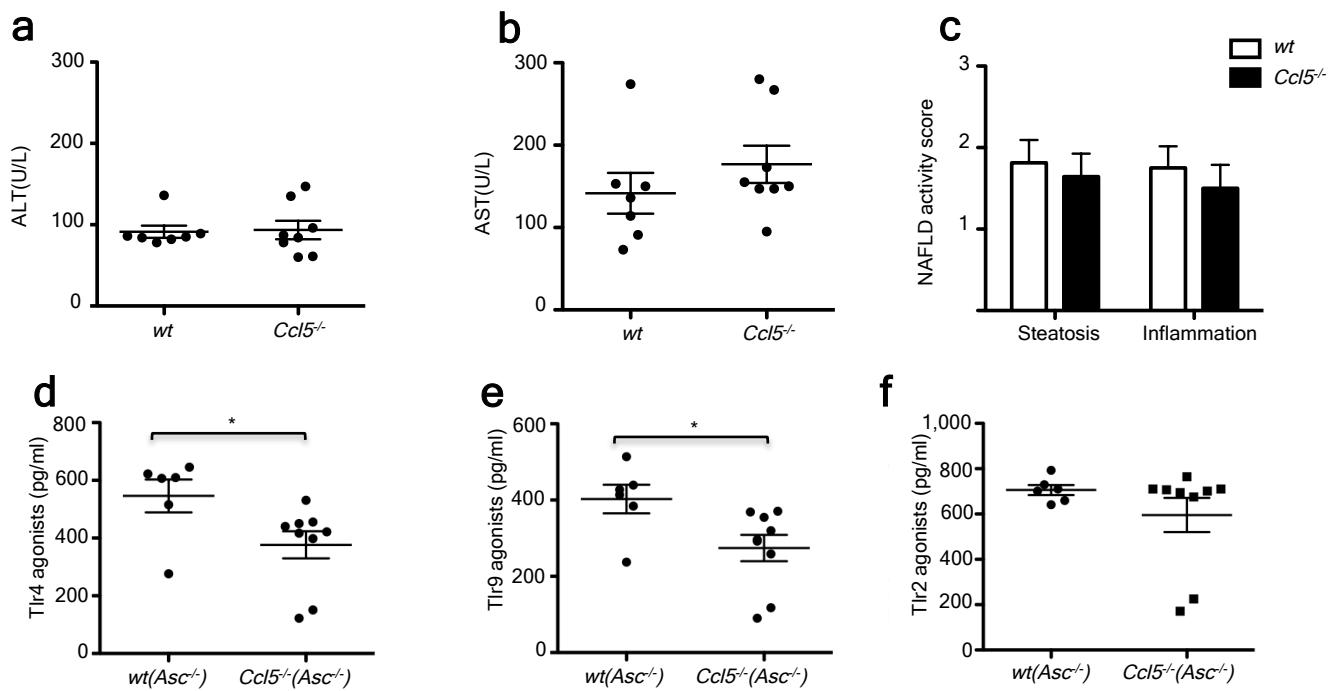
Supplemental figure 6. Increased severity of NASH in *Asc*-deficient mice and co-housed wild-type animals is mediated by TLR4, TLR9. *Asc*^{-/-} mice were co-housed with *wt*, *Myd88*^{-/-}; *Trif*^{-/-}, *Tlr4*^{-/-}, *Tlr9*^{-/-}, or *Tlr5*^{-/-} mice for 4 weeks, after which time mice were fed MCDD for 24 days to induce NASH. (a-b) Comparison of serum ALT and AST activities from MCDD-fed *wt*(*Asc*^{-/-}) and *Myd88*^{-/-}; *Trif*^{-/-}(*Asc*^{-/-}) mice. Data are representative of two independent experiments. (c-h) Comparison of serum AST levels and NAFLD activity histological scores for steatosis and inflammation from MCDD-fed *Tlr4*^{-/-}(*Asc*^{-/-}) (c-d), *Tlr9*^{-/-}(*Asc*^{-/-}) (e-f), and *Tlr5*^{-/-}(*Asc*^{-/-}) animals (g-h) and their singly-housed counterparts. Data represent two independent experiments. Error bars represent the SEM of samples within a group. *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001 (Student's t test).



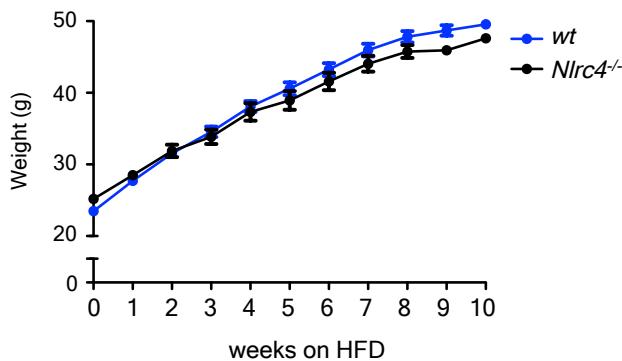
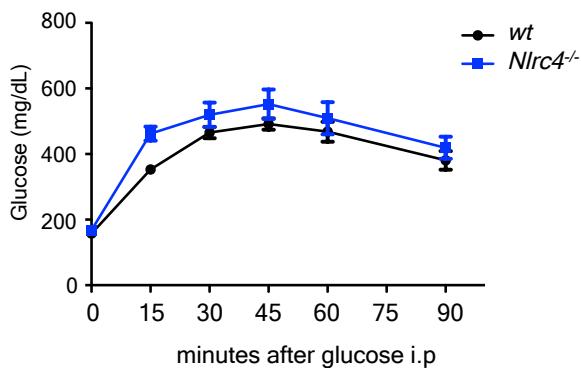
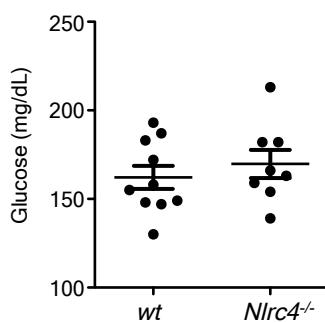
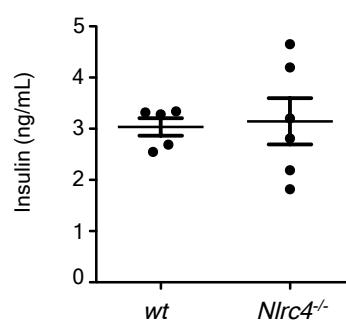
Supplemental figure 7. Increased severity of NASH in *Asc*-deficient mice and co-housed wild-type animals is mediated by TLR agonist influx into portal circulation. *Asc^{-/-}* mice were co-housed with *wt* mice for 4 weeks, after which time mice were fed MCDD for 24 days to induce NASH. (a-b) Comparison of TLR2 (a) and TLR9 (b) agonists in portal vein sera obtained at the time of sacrifice of singly-housed MCDD-fed *wt* mice, co-housed *wt(Asc^{-/-})* animals and singly-housed *Asc^{-/-}* animals. Data represent two independent experiments. (c) Representative transmission electron microscopy images taken from colonic sections prepared from *wt* (top X8200) and *Asc^{-/-}* animals (bottom left X16500). Error bars represent the SEM of samples within a group. *p≤0.05, **p≤ 0.01, ***p≤ 0.001. (ANOVA)



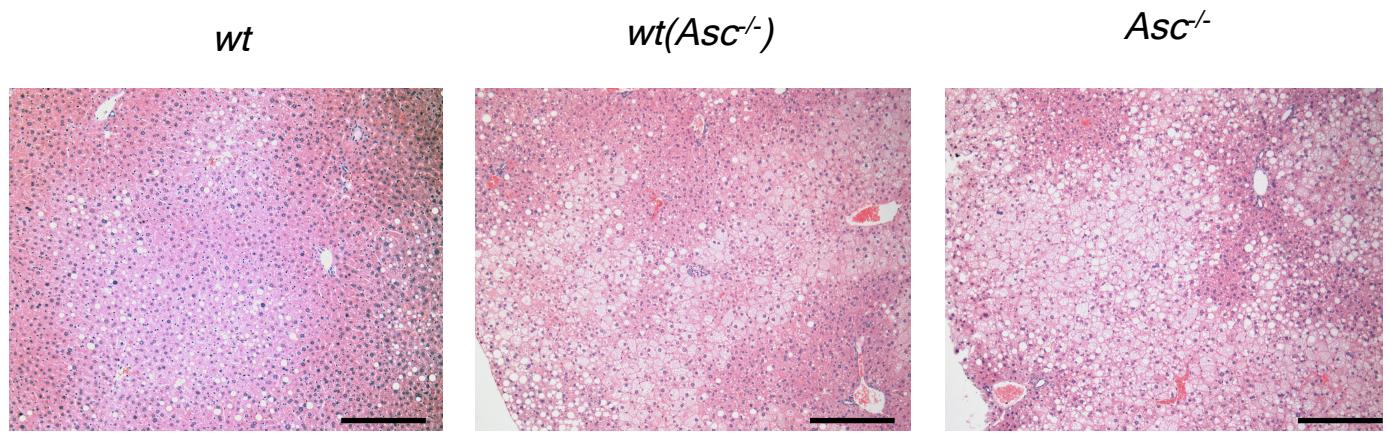
Supplemental figure 8. Increased *Tnfa* expression in *Asc^{-/-}*, *II18^{-/-}*, but not in *II1r^{-/-}* mice during NASH. (a-c) Comparison of hepatic *Tnfa*, *IL6*, and *IL1β* mRNA levels in singly-housed *wt* and *Asc^{-/-}*(a), *II18^{-/-}*(b), or *II1r^{-/-}*(c) mice. (d-e) Comparison of hepatic *Tnfa*, *IL6*, and *IL1β* mRNA levels in singly-housed *wt* mice (*wt*) versus *wt* mice that were previously co-housed with *Asc^{-/-}* animals (*wt(Asc^{-/-})*) (d), or *II18^{-/-}* animals (*wt(II18^{-/-})*)(e) for four weeks prior to NASH induction. (f-g) AST serum levels (f) and representative H&E-stained sections of livers from singly-housed *Tnfa^{-/-}* mice, and co-housed *wt* mice (*wt(Asc^{-/-})*) or *Tnfa^{-/-}* mice co-housed with *Asc^{-/-}* animals (*Tnfa^{-/-}(Asc^{-/-})*). Scale bars = 200 µm. Data are representative for two independent experiments. Error bars represent the SEM of samples within a group. *p≤ 0.05, **p≤ 0.01, ***p≤ 0.001. (Student's t test)



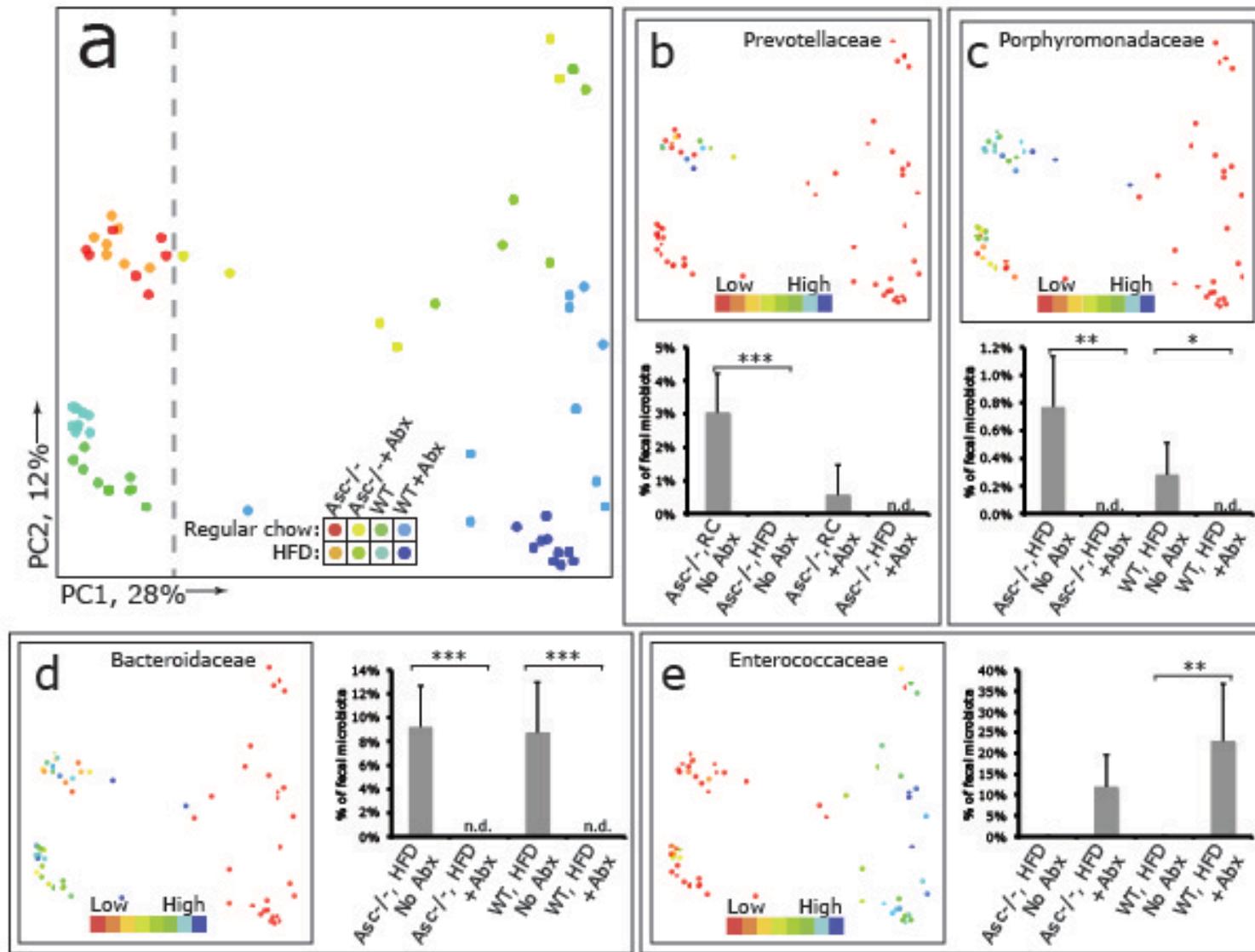
Supplementary figure 9. Intestinal inflammation associated with an *Asc*^{-/-} gut microbiota increases the influx of TLR agonists into the portal circulation. To induce NASH, mice were given MCDD for 24 d, and their serum ALT and AST activities, and NAFLD histological activity scores were determined. (a-c) Comparison of ALT (a), AST (b), and NAFLD activity histological scores (c) between separately housed *wt* and *Ccl5*^{-/-} mice. (n=8 animals surveyed/group). (d-f) *wt* or *Ccl5*^{-/-} mice were co-housed with *Asc*^{-/-} mice for 4 weeks after which time mice were fed MCDD for 24 d to induce NASH. Comparison of TLR4 (d), TLR9 (e), and TLR2 (f) agonists in portal vein sera collected from MCDD-treated, co-housed *wt(Asc*^{-/-}) and *Ccl5*^{-/-}(*Asc*^{-/-}) mice. Error bars represent the SEM of samples within a group (n=6 animals surveyed/group). *p≤0.05, **p≤0.01, ***p≤0.001 (Student's t test).

a**b****c****d**

Supplementary figure 10. *Nlrc4*-deficient mice have normal weight gain rate and glycemic control on HFD. Age-matched male *Nlrc4*^{-/-} mice and *wt* mice were fed a 60% HFD. Body weights were monitored weekly (a), glucose tolerance tests were performed in *wt* mice and *Nlrc4*^{-/-} mice after 10 weeks of HFD (b). Fasting (14h) blood glucose (c) and insulin (d) levels were measured after 8 weeks on the HFD, (n=8-10 mice/group). Error bars represent the SEM of samples within a group.



Supplemental figure 11. *Asc*-deficient mice co-housed *wt* mice develop increased steatosis on HFD. (a) Representative hematoxylin and eosin (H&E)-stained sections of livers from *wt*, *wt(Asc^{-/-})*, and *Asc^{-/-}* mice. Scale bars = 200 μ m.



Supplemental figure 12. Antibiotic treatment leads to reduction in taxa associated with HFD. (a) *Asc*-/- and WT mice were or were not treated with ciprofloxacin and metronidazole for 4 weeks before being switched to a high fat diet. Time points were taken after being fed HFD for 1 and 8 weeks. (b-e) PCoA and bar graphs showing reduction in Prevotellaceae, Porphyromonadaceae and Bacteroidaceae after antibiotic treatment. Enterococcaceae were noted to increase in representation after antibiotic treatment.

		Group				p values						Cohoused Cage p values				
		A ASC-/- (wt) & wt(ASC-/-) Regular diet (n=12)		B Singly housed wt Regular diet (n=8)		C ASC-/- (wt) & wt(ASC-/-) MCDD (n=12)		D Singly housed wt MCDD (n=8)		A vs B	B vs D*	B vs C*	A vs B	C vs D	MCDD	Reg
Phyla		Actinobacteria	0.1(0.06)	0.02(0.03)	0.08(0.07)	0.06(0.06)	0.06(0.06)	0.06(0.06)	0.06(0.06)	n.s.	n.s.	n.s.	3.5E-02	n.s.	n.s.	n.s.
		Bacteroidetes	52.01(10.83)	38.15(7.78)	32.72(7.71)	36.37(10.69)	37.58(11.05)	59.65(7.85)	53.95(10.83)	n.s.	n.s.	2.0E-02	1.2E-03	n.s.	n.s.	n.s.
		Firmicutes	37.58(11.05)	59.65(7.85)	53.95(10.83)	57.64(9.69)	32.72(7.71)	36.37(10.69)	37.58(11.05)	n.s.	n.s.	8.2E-03	n.s.	3.7E-02	n.s.	n.s.
		Proteobacteria	3.27(2.58)	0.18(0.28)	7.5(6.51)	0.71(0.32)	3.27(2.58)	0.18(0.28)	7.5(6.51)	n.s.	n.s.	2.8E-03	n.s.	1.5E-02	n.s.	n.s.
		Tenericutes	0.04(0.1)	0.07(0.07)	0.35(0.3)	0.2(0.16)	0.04(0.1)	0.07(0.07)	0.35(0.3)	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
		Verrucomicrobia	0.27(0.48)	0.06(0.07)	0.45(0.68)	2.17(2.19)	0.27(0.48)	0.06(0.07)	0.45(0.68)	n.s.	n.s.	n.s.	n.s.	n.s.	2.2E-08	5.9E-03
		Bacteroidetes; Bacteroides	20.68(5.76)	22.73(7.28)	28(7.54)	34.62(10.13)	20.68(5.76)	22.73(7.28)	28(7.54)	8.5E-03	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
Class		Bacteroidetes; Other	31.34(7.51)	15.41(8.86)	4.72(1.67)	1.75(1.1)	31.34(7.51)	15.41(8.86)	4.72(1.67)	4.3E-07	n.s.	1.7E-06	7.3E-03	6.0E-03	4.6E-02	n.s.
		Firmicutes; Bacilli	19.73(11.35)	42.79(15.8)	6.23(4.85)	4.98(6.05)	19.73(11.35)	42.79(15.8)	6.23(4.85)	1.5E-04	3.6E-03	1.5E-02	2.3E-02	n.s.	n.s.	n.s.
		Firmicutes; Erysipelotrichi	0.31(0.29)	0.39(0.66)	11.23(2.65)	11(4.95)	0.31(0.29)	0.39(0.66)	11.23(2.65)	2.1E-10	5.1E-03	2.6E-02	n.s.	n.s.	4.5E-02	n.s.
		Firmicutes; Other	4.4(5.83)	1.13(0.52)	18.79(12.11)	23.15(18.62)	4.4(5.83)	1.13(0.52)	18.79(12.11)	1.1E-03	n.s.	3.5E-02	n.s.	n.s.	n.s.	1.7E-02
		Proteobacteria; Deltaproteobacteria	0.79(0.86)	0.13(0.23)	0.75(0.45)	0.53(0.28)	0.79(0.86)	0.13(0.23)	0.75(0.45)	n.s.	n.s.	1.8E-02	n.s.	n.s.	n.s.	n.s.
		Tenericutes; Mollicutes	0.04(0.1)	0.07(0.07)	0.35(0.3)	0.2(0.16)	0.04(0.1)	0.07(0.07)	0.35(0.3)	5.1E-03	n.s.	2.6E-02	n.s.	n.s.	n.s.	n.s.
		Verrucomicrobia; Verrucomicrobiae	0.27(0.48)	0.06(0.07)	0.45(0.68)	2.17(2.19)	0.27(0.48)	0.06(0.07)	0.45(0.68)	n.s.	n.s.	n.s.	n.s.	n.s.	4.0E-08	1.1E-02
Order		Bacteroidetes; Bacteroides; Bacteroidales	20.68(5.76)	22.73(7.28)	28(7.54)	34.62(10.13)	20.68(5.76)	22.73(7.28)	28(7.54)	1.1E-02	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
		Firmicutes; Bacilli; Lactobacillales	19.71(11.36)	42.77(15.8)	5.89(4.6)	4.94(6.05)	19.71(11.36)	42.77(15.8)	5.89(4.6)	1.4E-04	4.6E-03	1.2E-02	3.1E-02	n.s.	n.s.	n.s.
		Firmicutes; Clostridia; Other	0.01(0.03)	0.01(0.01)	0.04(0.03)	0.07(0.06)	0.01(0.03)	0.01(0.01)	0.04(0.03)	5.8E-03	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
		Firmicutes; Erysipelotrichi; Erysipelotrichales	0.31(0.29)	0.39(0.66)	11.23(2.65)	11(4.95)	0.31(0.29)	0.39(0.66)	11.23(2.65)	2.8E-10	6.8E-03	3.4E-07	n.s.	n.s.	n.s.	n.s.
		Proteobacteria; Deltaproteobacteria; Desulfovibrionales	0.01(0.03)	0.04(0.05)	0.21(0.16)	0.2(0.15)	0.01(0.03)	0.04(0.05)	0.21(0.16)	1.4E-03	n.s.	4.1E-02	n.s.	n.s.	n.s.	n.s.
		Tenericutes; Mollicutes; Anaeroplasmatales	0(0)	0.07(0.07)	0(0)	0.2(0.16)	0(0)	0.07(0.07)	0(0)	n.s.	n.s.	n.d.	5.3E-03	n.d.	n.d.	n.d.
		Tenericutes; Mollicutes; Other	0.02(0.05)	0(0)	0.17(0.09)	0(0)	0.02(0.05)	0(0)	0.17(0.09)	2.3E-02	n.d.	3.8E-03	n.s.	1.1E-03	n.s.	n.s.
Family		Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales	0.27(0.48)	0.06(0.07)	0.45(0.68)	2.17(2.19)	0.27(0.48)	0.06(0.07)	0.45(0.68)	n.s.	n.s.	n.s.	n.s.	n.s.	5.3E-08	1.4E-02
		Bacteroides; Bacteroides; Bacteroidales; Bacteroidaceae	2.6(1.09)	9.64(5.04)	1.97(1.14)	25.7(8.87)	2.6(1.09)	9.64(5.04)	1.97(1.14)	n.s.	9.2E-03	n.s.	6.1E-03	1.0E-06	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Porphyromadaceae	0.78(0.55)	0.02(0.02)	5.76(3.29)	0.16(0.08)	0.78(0.55)	0.02(0.02)	5.76(3.29)	n.s.	2.0E-02	2.2E-02	4.3E-02	5.6E-03	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Prevotellaceae	1.6(1.64)	0(0)	0.1(0.06)	0(0)	1.6(1.64)	0(0)	0.1(0.06)	n.s.	n.d.	n.s.	n.s.	1.0E-02	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Rikenellaceae	5.82(3.71)	5.31(4.59)	8.61(2.12)	1.59(0.79)	5.82(3.71)	5.31(4.59)	8.61(2.12)	n.s.	n.s.	n.s.	n.s.	1.9E-06	n.s.	9.1E-03
		Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae	19.59(11.33)	42.67(15.81)	5.63(4.45)	4.84(5.99)	19.59(11.33)	42.67(15.81)	5.63(4.45)	1.9E-04	7.2E-03	1.6E-02	4.7E-02	n.s.	n.s.	n.s.
		Firmicutes; Clostridia; Clostridiales; Lachnospiraceae	9.65(4.81)	9.15(5.92)	6.8(2.35)	9.54(3.55)	9.65(4.81)	9.15(5.92)	6.8(2.35)	n.s.	n.s.	n.s.	n.s.	n.s.	5.5E-03	n.s.
Genus		Firmicutes; Clostridia; Clostridiales; Peptostreptococcaceae	0(0)	0(0)	1.88(1.09)	0.68(1.01)	0(0)	0(0)	1.88(1.09)	1.7E-03	n.s.	3.4E-03	n.d.	n.s.	2.9E-02	n.d.
		Firmicutes; Clostridia; Clostridiales; Other	1.73(0.54)	4.85(7.41)	3.62(1.54)	4.6(1.18)	1.73(0.54)	4.85(7.41)	3.62(1.54)	n.s.	n.s.	1.9E-02	n.s.	n.s.	n.s.	n.s.
		Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae	0.31(0.29)	0.39(0.66)	11.23(2.65)	11(4.95)	0.31(0.29)	0.39(0.66)	11.23(2.65)	4.3E-10	1.0E-02	5.2E-07	n.s.	n.s.	n.s.	n.s.
		Proteobacteria; Deltaproteobacteria; Desulfovibrionales	0.01(0.03)	0.04(0.05)	0.21(0.16)	0.2(0.15)	0.01(0.03)	0.04(0.05)	0.21(0.16)	2.2E-03	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
		Tenericutes; Mollicutes; Anaeroplasmatales; Anaeroplasmataceae	0(0)	0.07(0.07)	0(0)	0.2(0.16)	0(0)	0.07(0.07)	0(0)	n.s.	n.s.	n.d.	n.s.	8.2E-03	n.d.	n.d.
		Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiaceae	0.27(0.48)	0.06(0.07)	0.45(0.68)	2.17(2.19)	0.27(0.48)	0.06(0.07)	0.45(0.68)	n.s.	n.s.	n.s.	n.s.	n.s.	8.2E-08	2.2E-02
		Bacteroides; Bacteroides; Bacteroidales; Bacteroidaceae; Bacteroides	2.6(1.09)	9.64(5.04)	1.97(1.14)	25.7(8.87)	2.6(1.09)	9.64(5.04)	1.97(1.14)	3.0E-04	1.1E-02	2.4E-02	n.s.	n.s.	1.6E-06	n.s.
Firmicutes		Bacteroides; Bacteroides; Bacteroidales; Porphyromadaceae; Parabacteroides	0.78(0.55)	0.02(0.02)	5.76(3.29)	0.16(0.08)	0.78(0.55)	0.02(0.02)	5.76(3.29)	n.s.	3.2E-02	3.4E-02	n.s.	8.6E-03	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Prevotellaceae; Prevotella	1.53(1.57)	0(0)	0.1(0.06)	0(0)	1.53(1.57)	0(0)	0.1(0.06)	n.s.	n.d.	n.s.	n.s.	1.3E-02	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Rikenellaceae; Alistipes	1.69(1.1)	0.77(0.37)	3.92(2.24)	0.54(0.45)	1.69(1.1)	0.77(0.37)	3.92(2.24)	n.s.	n.s.	n.s.	n.s.	3.3E-02	n.s.	n.s.
		Bacteroides; Bacteroides; Bacteroidales; Rikenellaceae; Other	4.04(2.86)	4.54(4.68)	4.49(1.98)	1.04(0.92)	4.04(2.86)	4.54(4.68)	4.49(1.98)	n.s.	n.s.	n.s.	n.s.	1.4E-02	n.s.	1.7E-02
		Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus	19.59(11.33)	42.67(15.81)	5.63(4.45)	4.84(5.99)	19.59(11.33)	42.67(15.81)	5.63(4.45)	3.0E-04	1.1E-02	2.4E-02	n.s.	n.s.	n.s.	n.s.
		Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Other	9.25(4.98)	8.27(5.68)	6.25(2.12)	8.82(3.5)	9.25(4.98)	8.27(5.68)	6.25(2.12)	n.s.	n.s.	n.s.	n.s.	n.s.	5.4E-03	n.s.
		Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridiaceae 1	0(0)	0(0)	1.88(1.09)	0.68(1.01)	0(0)	0(0)	1.88(1.09)	2.7E-03	n.s.	5.3E-03	n.d.	n.s.	n.s.	n.d.
Proteobacteria		Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; Turicibacter	0.01(0.04)	0.28(0.63)	3.22(3.59)	1.9(0.62)	0.01(0.04)	0.28(0.63)	3.22(3.59)	3.7E-02	2.6E-04	n.s.	n.s.	n.s.	4.4E-02	n.s.
		Tenericutes; Mollicutes; Anaeroplasmatales; Desulfovibrionaceae; Other	0(0.01)	0.04(0.05)	0.1(0.1)	0.2(0.15)	0(0.01)	0.04(0.05)	0.1(0.1)	2.0E-02	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
		Tenericutes; Mollicutes; Anaeroplasmatales; Anaeroplasmataceae; Anaeroplasma	0(0)	0.07(0.07)	0(0)	0.2(0.16)	0(0)	0.07(0.07)	0(0)	n.s.	n.s.	n.d.	n.s.	1.3E-02	n.d.	n.d.
		Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Verrucomicrobiaceae; Akkermansia	0.27(0.48)	0.06(0.07)	0.45(0.68)	2.17(2.19)	0.27(0.48)	0.06(0.07)	0.45(0.68)	n.s.	n.s.	n.s.	n.s.	n.s.	1.3E-07	3.4E-02

Supplemental Table 1
Average bacterial taxonomic representation of Asc-/- (wt) and wt(Asc-/-) or singly housed mice fed a regular or MCDD (See also figure 3). Values are expressed as averages per group with standard deviation in parentheses. P values, as determined by t test and corrected for multiple hypothesis testing by Bonferroni correction, are shown comparing groups.

		Group								p values									
		A	B	C	D	E	F	G	H	A vs C	B vs D	E vs G	F vs H	A vs B	E vs F	A vs E	B vs F	G vs H	
Phyla	Actinobacteria	ASC wk1	ASC wk8	ASC+abx wk1	ASC+abx wk8	WT wk1	WT wk8	WT+abx wk1	WT+abx wk8	n.s.	n.s.	1.2E-03	n.s.	n.s.	7.8E-03	n.s.	1.9E-03		
		0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	2.4E-04	n.s.	4.8E-05	4.0E-06	n.s.	n.s.	n.s.	
		58.61(5.1)	27.45(9.25)	37.8(41.47)	8.88(12.92)	57.07(10.24)	22.22(8.67)	12.08(23.09)	16.03(11.21)	n.s.	n.s.	8.0E-04	2.3E-03	7.3E-04	4.9E-06	n.s.	n.s.	3.8E-03	
		28.47(8.21)	60.16(11.61)	58.35(43.22)	52.32(17.97)	40.88(10.18)	73.76(7.82)	84.29(25.1)	39.3(20.92)	n.s.	2.0E-04	4.3E-05	7.0E-05	n.s.	n.s.	5.7E-03	n.s.		
		6.5(5.41)	4.33(1.63)	1.5(2.12)	0.1(0.27)	1.33(0.34)	1.67(0.69)	0.21(0.43)	0.26(0.11)	n.s.	1.5E-02	2.0E-02	1.2E-02	n.s.	2.0E-02	3.4E-03	n.s.	n.d.	
	Proteobacteria	5.73(3.92)	2.72(0.83)	1.63(1.62)	31.77(18.7)	0.09(0.08)	1.48(1.21)	0(0)	0(0)	n.s.	1.3E-02	n.s.	n.d.	n.s.	3.3E-03	3.0E-03	n.s.		
		0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0.01)	0(0)	n.s.	n.s.	n.s.	3.4E-04	n.s.	n.s.	n.s.	5.6E-04		
		0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	2.2E-03	n.s.	n.s.	1.4E-02	n.s.	3.4E-03		
		0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	1.5E-04	4.1E-03	8.3E-03	n.s.	4.3E-05	n.s.	n.s.	n.s.	
		31.59(8.05)	21.64(7.75)	31.91(34.56)	0(0)	45.74(9.52)	18.19(7.53)	11.34(21.69)	5.73(4.87)	n.s.	3.4E-06	n.s.	7.5E-03	1.1E-03	1.9E-02	n.s.	1.6E-02		
Class	Verrucomicrobia	Bacteroidetes;Actinobacteria	Bacteroidetes;Bacteroidetes	Bacteroidetes;Other	27.02(11.47)	5.8(1.9)	5.89(8.67)	8.88(12.92)	11.34(3.87)	4.03(1.53)	0.73(1.42)	10.3(7.51)	n.s.	1.1E-03	n.s.	n.s.	5.2E-02		
		Firmicutes;Bacilli	8.99(6.72)	12.62(11.86)	52.87(48.81)	24.52(19.23)	23.01(15.72)	19.62(9.75)	81.39(31.93)	36.77(19.43)	n.s.	1.0E-05	4.0E-02	1.7E-09	2.4E-03	9.9E-06	n.s.	n.s.	
		Firmicutes;Clostridia	17.81(8.64)	43.24(8.63)	4.45(4.82)	2.89(7.05)	15.55(9.3)	53.25(11.84)	2.29(7.18)	1.03(0.67)	n.s.	n.s.	9.2E-03	9.8E-03	n.s.	2.2E-02	n.s.	5.1E-04	
		Firmicutes;Erysipelotrichi	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	n.d.	4.4E-03	n.d.	n.s.	8.6E-03	n.d.	n.d.	
		Proteobacteria;Beta-proteobacteria	0.05(0.07)	0(0)	0(0)	0(0)	0.05(0.04)	0(0)	0(0)	0(0)	n.s.	1.9E-02	n.d.	n.d.	n.s.	7.1E-03	2.6E-07	n.d.	
	TM7	Proteobacteria;Epsilonproteobacteria	5.07(3.58)	1.43(0.37)	1.58(1.59)	31.77(18.7)	0(0)	0(0)	0(0)	0(0)	n.s.	2.3E-02	n.s.	n.d.	n.s.	6.0E-03	5.3E-03	n.s.	
		TM7;TM7_genera_Incertae_sedis	0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0.01)	0(0)	n.s.	n.s.	6.2E-04	n.s.	n.s.	n.s.	1.0E-03		
		Verrucomicrobia;Verrucomicrobiales	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	2.9E-03	n.s.	n.s.	1.9E-02	n.s.	4.5E-03	
		Actinobacteria;Actinobacteridae;Coriobacteridae	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	2.0E-04	5.4E-03	1.1E-02	n.s.	5.7E-05	n.s.	n.s.	
		Bacteroidetes;Bacteroidetes;Bacteroidales	31.59(8.05)	21.64(7.75)	31.91(34.56)	0(0)	45.74(9.52)	18.19(7.53)	11.34(21.69)	5.73(4.87)	n.s.	n.s.	4.6E-06	n.s.	9.9E-03	1.4E-03	2.5E-02	n.s.	2.2E-02
Order	Actinobacteria	Bacteroidetes;Other;Other	27.02(11.47)	5.8(1.9)	5.89(8.67)	8.88(12.92)	11.34(3.87)	4.03(1.53)	0.73(1.42)	10.3(7.51)	n.s.	1.5E-03	n.s.	n.s.	n.s.	n.s.	3.3E-02		
		Firmicutes;Bacilli;Lactobacillales	8.99(6.72)	12.6(11.87)	52.87(48.81)	24.51(19.22)	23.01(15.73)	19.53(9.81)	81.39(31.93)	36.77(19.43)	n.s.	1.4E-05	3.8E-02	2.1E-09	3.3E-03	1.2E-05	n.s.	n.s.	
		Firmicutes;Clostridia;Clostridiales	17.81(8.64)	43.14(8.58)	4.45(4.82)	2.89(7.05)	15.48(9.22)	53.08(11.74)	2.12(6.65)	1.03(0.67)	n.s.	n.s.	1.2E-02	1.3E-02	n.s.	2.9E-02	n.s.	6.8E-04	
		Firmicutes;Erysipelotrichi;Erysipelotrichales	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	n.d.	5.9E-03	n.d.	n.s.	1.1E-02	n.d.	n.d.	
		Proteobacteria;Epsilonproteobacteria;Campylobacteriales	0.05(0.07)	0(0)	0(0)	0(0)	0.05(0.04)	0(0)	0(0)	0(0)	n.s.	2.5E-02	n.d.	n.d.	n.s.	9.4E-03	3.4E-07	n.d.	
	Verrucomicrobia	TM7;TM7_genera_Incertae_sedis;Other	0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0.01)	0(0)	n.s.	3.1E-02	n.s.	n.d.	n.s.	8.0E-03	7.1E-03	n.s.	
		Verrucomicrobia;Verrucomicrobia;Verrucomicrobiales	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	8.2E-04	n.s.	n.s.	n.s.	1.3E-03		
		Actinobacteria;Actinobacteria;Coriobacteridae;Coriobacteriales	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	4.4E-03	n.s.	n.s.	n.s.	2.9E-02	n.s.	6.9E-03	
		Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae	0.62(0.18)	9.24(3.49)	8.95(13.02)	0(0)	5.23(1.92)	8.76(4.22)	2.76(8.73)	0(0)	n.s.	5.3E-04	n.s.	1.7E-04	1.1E-03	n.s.	5.6E-04	n.s.	
		Bacteroidetes;Bacteroidetes;Bacteroidales;Other	15.97(4.14)	5.18(4.73)	11.73(12.86)	0(0)	22.49(5.31)	7.25(3.21)	7.14(10.83)	5.73(4.86)	n.s.	2.9E-02	n.s.	2.5E-05	n.s.	n.s.	n.s.	n.s.	
Family	Actinobacteria	Bacteroidetes;Bacteroidetes;Bacteroidales;Prevotellaceae	3.05(1.18)	0.01(0.02)	0.57(0.59)	0(0)	0(0)	0(0)	0(0)	0(0)	n.s.	n.d.	6.7E-04	n.d.	6.7E-04	n.d.	2.0E-05	n.s.	
		Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae	10.94(3.75)	6.45(2.52)	5.61(12.7)	0(0)	17.97(7.67)	1.9(0.95)	1.44(3.81)	0(0.01)	n.s.	7.2E-04	3.4E-04	2.7E-04	n.s.	3.4E-04	n.s.	6.9E-03	
		Firmicutes;Bacilli;Lactobacillales;Enterococcaceae	0(0)	0.02(0.03)	0.02(0.04)	11.88(7.61)	0(0.01)	0.11(0.09)	43.17(35.8)	22.99(13.62)	n.s.	4.7E-02	3.8E-03	n.s.	n.s.	n.s.	n.s.	n.s.	
		Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	0(0.01)	2.44(0.81)	0.01(0.02)	9.11(11.45)	0(0)	4.86(2.53)	0(0)	9.8(5.18)	n.s.	n.s.	n.d.	n.s.	1.6E-04	4.4E-04	n.s.	4.4E-04	
		Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	8(6.17)	23.23(12.3)	3.83(4.19)	1.27(3.34)	4.71(3.19)	29.59(7.33)	1.69(5.31)	0(0.01)	n.s.	2.4E-02	n.s.	1.4E-08	n.s.	8.0E-07	n.s.	n.s.	
	Proteobacteria	Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	13.04(3.84)	4.57(1.75)	0.25(0.33)	0.42(0.69)	1.37(0.67)	4.78(1.91)	0.06(0.2)	1.03(0.67)	n.s.	3.0E-03	4.9E-04	7.2E-04	3.1E-02	2.1E-03	n.s.	1.3E-02	
		Firmicutes;Clostridia;Clostridiales;Uncultured	0.01(0.04)	0.16(0.16)	0.02(0.04)	0(0)	0.01(0.02)	0.18(0.12)	0(0)	0(0)	n.s.	n.s.	6.0E-03	n.s.	1.4E-02	n.s.	n.d.		
		Firmicutes;Clostridia;Clostridiales;Other	3.19(2.78)	10.79(5.97)	0.35(0.65)	1.19(3.16)	4.01(2.95)	16.13(5.32)	0.36(3.12)	0(0)	n.s.	1.9E-02	2.0E-02	n.s.	4.4E-02	n.s.	1.0E-03		
		Firmicutes;Erysipelotrichi;Erysipelotrichales	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	3.9E-02	n.d.	n.s.	n.d.	1.5E-02	5.3E-07	n.d.	
		Proteobacteria;Epsilonproteobacteria;Campylobacteriales	5.07(3.58)	1.43(0.37)	1.58(1.59)	31.77(18.7)	0(0)	0(0)	0(0)	0(0)	n.s.	6.8E-03	n.s.	1.3E-03	n.s.	n.s.	2.1E-03		
Genus	Actinobacteria	Verrucomicrobia;Verrucomicrobia;Verrucomicrobiales	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	6.8E-03	n.s.	4.5E-02	n.s.	1.5E-02		
		Actinobacteria;Actinobacteridae;Coriobacteridae	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	8.2E-04	n.s.	2.7E-04	1.6E-03	n.s.	n.s.	
		Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae	0.62(0.18)	9.24(3.49)	8.95(13.02)	0(0)	5.23(1.92)	8.76(4.22)	2.76(8.73)	0(0)	n.s.	6.8E-03	n.s.	1.3E-03	n.s.	4.5E-02	n.s.		
		Bacteroidetes;Bacteroidetes;Parabacteroides;Parabacteroides	1.02(0.34)	0.77(0.37)	5.06(6.18)	0(0)	0.05(0.04)	0.28(0.23)	0(0)	0(0)	n.s.	n.s.	6.8E-03	n.s.	n.s.	8.8E-06	n.s.		
		Bacteroidetes;Bacteroidetes;Prevotellaceae;Other	0.11(0.07)	0(0)	0.01(0.02)	0(0)	0(0)	0(0)	0(0)	0(0)	n.s.	n.d.	n.d.	n.d.	n.d.	1.2E-02	n.d.		
	Firmicutes	Bacteroidetes;Bacteroidetes;Prevotellaceae	2.94(1.18)	0.01(0.02)	0.56(0.88)	0(0)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	6.2E-04	n.d.	1.5E-03	n.d.	5.1E-05	n.s.	
		Bacteroidetes;Bacteroidetes;Rikenellaceae;Alistipes	1.14(0.72)	4.61(1.89)	0(0)	0(0)	0.73(0.37)	1.88(0.96)	0(0)	0(0)	n.s.	1.8E-03	4.1E-04	5.3E-04	3.9E-02	n.s.	n.s.		
		Bacteroidetes;Bacteroidetes;Ruminococcaceae;Other	9.78(6.87)	1.84(1.21)	5.59(12.66)	0(0)	17.24(7.68)	0.02(0.04)	1.44(3.81)	0(0.01)	n.s.	9.2E-04	n.s.	n.s.	2.1E-04	n.s.	2.6E-02		
		Firmicutes;Bacilli;Lactobacillales;Enterococcaceae	0(0)	0.02(0.03)	0.02(0.04)	11.64(7.44)	0(0.01)	0.11(0.09)	43.04(35.75)	22.92(13.59)	n.s.	n.s.	6.0E-03	n.s.	n.s.	n.s.	n.s.		
		Firmicutes;Bacilli;Lactobacillales;Streptococcaceae;Lactococcus	0(0)	2.4(0.81)	0.01(0.02)	9.1(11.45)	0(0)	4.86(2.53)	0(0)	9.8(5.18)	n.s.	n.s.	2.7E-04	6.8E-04	n.d.	n.s.	6.7E-04		
Firmicutes	Clostridia	Firmicutes;Clostridia;Lachnospiraceae;Lachnospiraceae	0.29(0.22)	0.94(0.41)	0.43(0.51)	0(0)	0.56(0.46)	1.51(1.24)	0.05(0.16)	0(0)	n.s.	3.0E-03	n						

			Group								p values											
			A	B	C	D	E	F	G	H	A vs B	B vs D	E vs G	F vs H	A vs C	E vs F	A vs E	B vs F	G vs H			
			ASC-/- Reg chow	ASC-/- HFD	ASC-/- +abx Reg chow	ASC-/- +abx HFD	WT Reg chow	WT HFD	WT+abx Reg chow	WT+abx HFD	n.s.	n.s.	1.2E-03	n.s.	n.s.	7.8E-03	n.s.	1.9E-03				
Phyla			Actinobacteria	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	2.4E-04	n.s.	4.8E-05	4.0E-06	n.s.	n.s.	n.s.	n.s.	
			Bacteroidetes	58.61(5.1)	27.45(9.25)	37.8(41.47)	8.88(12.92)	57.07(10.24)	22.22(8.67)	12.08(23.09)	16.03(11.21)	n.s.	n.s.	8.0E-04	2.3E-03	7.3E-04	4.9E-06	n.s.	n.s.	3.8E-03		
			Firmicutes	28.47(8.21)	60.16(11.61)	58.35(43.22)	52.32(17.97)	40.88(10.18)	73.76(7.82)	84.29(25.1)	39.3(20.92)	n.s.	n.s.	2.0E-04	4.3E-05	7.0E-05	n.s.	n.s.	5.7E-03	n.s.		
			Other	6.5(5.41)	4.33(1.63)	1.5(2.12)	0.1(0.27)	1.33(0.34)	1.67(0.69)	0.21(0.43)	0.26(0.11)	n.s.	n.s.	1.5E-02	2.0E-02	1.2E-02	n.s.	2.0E-02	3.4E-03	n.s.		
			Proteobacteria	5.73(3.92)	2.72(0.83)	1.63(1.62)	31.77(18.7)	0.09(0.08)	1.48(1.21)	0(0)	0(0)	n.s.	n.s.	1.3E-02	n.s.	n.d.	n.s.	n.d.	3.3E-03	3.0E-03	n.s.	
			TM7	0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	5.6E-04			
			Verrucomicrobia	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	3.4E-04	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	3.4E-03		
			Actinobacteria;Actinobacteria	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	2.2E-03	n.s.	n.s.	n.s.	1.4E-02	n.s.	3.4E-03		
			Bacteroidetes;Bacteroides	31.59(8.05)	21.64(7.75)	31.91(34.56)	0(0)	45.74(9.52)	18.19(7.53)	11.34(21.69)	5.73(4.87)	n.s.	n.s.	1.5E-04	4.1E-03	8.3E-03	n.s.	4.3E-05	n.s.	n.s.		
			Bacteroidetes;Other	27.02(11.47)	5.8(1.9)	5.89(6.67)	8.88(12.92)	11.34(3.87)	4.03(1.53)	0.73(1.42)	10.3(7.51)	n.s.	n.s.	3.4E-06	n.s.	7.5E-03	1.1E-03	1.9E-02	n.s.	1.6E-02		
Class			Firmicutes;Bacilli	8.99(6.72)	12.62(11.86)	52.87(48.81)	24.52(19.23)	23.01(15.72)	19.62(9.75)	81.39(31.93)	36.77(19.43)	n.s.	n.s.	1.1E-03	n.s.	n.s.	n.s.	n.s.	n.s.	2.5E-02		
			Firmicutes;Clostridia	17.81(8.64)	43.24(8.63)	4.45(4.82)	2.89(7.05)	15.55(9.3)	53.25(11.84)	2.29(7.18)	1.03(0.67)	n.s.	n.s.	1.0E-05	4.0E-02	1.7E-09	2.4E-03	9.9E-06	n.s.	n.s.		
			Firmicutes;Erysipelotrichi	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	n.s.	9.2E-02	n.s.	n.s.	n.s.	n.s.	n.s.	5.1E-04		
			Proteobacteria;Betaproteobacteria	0.05(0.07)	0(0)	0(0)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	4.4E-03	n.d.	8.6E-03	n.s.	n.s.	n.s.	n.d.			
			Proteobacteria;Epsilonproteobacteria	5.07(3.58)	1.43(0.37)	1.58(1.59)	31.77(18.7)	0(0)	0(0)	0(0)	n.s.	n.s.	1.9E-02	n.d.	7.1E-03	2.6E-07	n.d.	n.s.	n.s.			
			TM7;TM7_genra_incertae_sedis	0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	2.3E-02	n.s.	n.d.	n.d.	6.0E-03	5.3E-03	n.s.			
			Verrucomicrobia;Verrucomicrobiae	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	6.2E-04	n.s.	n.s.	n.s.	n.s.	n.s.	1.0E-03			
			Actinobacteria;Actinobacteria;Coriobacteriidae	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	2.9E-03	n.s.	n.s.	n.s.	1.9E-02	n.s.	4.5E-03		
			Bacteroidetes;Bacteroides;Bacteroidales	31.59(8.05)	21.64(7.75)	31.91(34.56)	0(0)	45.74(9.52)	18.19(7.53)	11.34(21.69)	5.73(4.87)	n.s.	n.s.	2.0E-04	5.4E-03	1.1E-02	n.s.	5.7E-05	n.s.	n.s.		
			Bacteroidetes;Other;Other	27.02(11.47)	5.8(1.9)	5.89(6.67)	8.88(12.92)	11.34(3.87)	4.03(1.53)	0.73(1.42)	10.3(7.51)	n.s.	n.s.	4.6E-06	n.s.	9.9E-03	1.4E-03	2.5E-02	n.s.	2.2E-02		
Order			Firmicutes;Bacilli;Lactobacillales	8.99(6.72)	12.6(11.87)	52.87(48.81)	24.51(19.22)	23.01(15.73)	19.53(9.81)	81.39(31.93)	36.77(19.43)	n.s.	n.s.	1.5E-03	n.s.	n.s.	n.s.	n.s.	n.s.	3.3E-02		
			Firmicutes;Clostridia;Clostridiales	17.81(8.64)	43.14(8.58)	4.45(4.82)	2.89(7.05)	15.48(9.22)	53.08(11.74)	2.12(6.65)	1.03(0.67)	n.s.	n.s.	1.4E-05	3.8E-02	2.1E-09	3.3E-03	1.2E-05	n.s.	n.s.		
			Firmicutes;Erysipelotrichi;Erysipelotrichales	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	n.s.	1.2E-02	1.3E-02	3.2E-02	n.s.	2.9E-02	n.s.	6.8E-04		
			Proteobacteria;Betaproteobacteria;Other	0.05(0.07)	0(0)	0(0)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	5.9E-03	n.d.	n.s.	1.1E-02	n.s.	n.d.	n.d.			
			Proteobacteria;Epsilonproteobacteria;Campylobacterales	5.07(3.58)	1.43(0.37)	1.58(1.59)	31.77(18.7)	0(0)	0(0)	0(0)	n.s.	n.s.	2.5E-02	n.d.	n.d.	n.s.	9.4E-03	3.4E-07	n.d.			
			TM7;TM7_genra_incertae_sedis;Other	0.41(0.29)	1.95(1.24)	0.07(0.18)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	3.1E-02	n.d.	n.d.	n.s.	8.0E-03	7.1E-03	n.s.			
			Verrucomicrobie;Verrucomicrobiae;Verrucomicrobiales	0.05(0.11)	2.77(4.03)	0.4(0.69)	2.68(4)	0(0.01)	3.37(6.58)	44.15(23.73)	n.s.	n.s.	8.2E-04	n.s.	n.s.	n.s.	n.s.	n.s.	1.3E-03			
			Actinobacteria;Actinobacteria;Coriobacteriales	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	4.4E-03	n.s.	n.s.	2.9E-02	n.s.	6.9E-03			
			Bacteroidetes;Bacteroides;Bacteroidaceae	0.62(0.18)	9.24(3.49)	8.95(13.02)	0(0)	5.23(1.92)	8.76(4.22)	2.76(8.73)	0(0)	n.s.	5.3E-04	n.s.	1.7E-04	1.1E-03	5.6E-04	n.s.	n.s.			
			Bacteroidetes;Bacteroides;Bacteroidales;Other	15.97(4.19)	51.84(7.43)	11.73(12.86)	0(0)	22.49(5.31)	7.25(3.21)	7.14(10.83)	5.73(4.86)	n.s.	n.s.	2.9E-02	n.s.	2.5E-02	3.5E-05	n.s.	n.s.			
Family			Bacteroidetes;Bacteroides;Bacteroidales;Porphyromonadaceae	1.02(0.34)	0.77(0.37)	5.06(6.18)	0(0)	0.05(0.04)	0.28(0.23)	0(0)	0(0)	n.s.	n.s.	4.4E-03	n.s.	4.5E-02	n.s.	5.7E-06	n.s.	n.d.		
			Bacteroidetes;Bacteroides;Bacteroidales;Prevotellaceae	3.05(1.18)	0.01(0.02)	0.57(0.9)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	n.d.	n.d.	6.7E-04	n.d.	2.0E-05	n.s.	n.d.			
			Bacteroidetes;Bacteroides;Bacteroidales;Rikenellaceae	10.94(7.35)	6.45(2.52)	5.61(12.7)	0(0)	17.97(7.67)	0(0.95)	1.44(3.81)	0(0.01)	n.s.	n.s.	7.2E-04	3.4E-04	2.7E-04	n.s.	3.4E-04	n.s.	6.9E-03		
			Firmicutes;Bacilli;Lactobacillales;Enterococcaceae	0(0)	0.02(0.03)	0.02(0.04)	11.88(7.61)	0(0.01)	0.11(0.09)	43.17(35.8)	22.99(13.62)	n.s.	n.s.	4.7E-02	3.8E-03	n.s.	n.s.	n.s.	n.s.	n.s.		
			Firmicutes;Bacilli;Lactobacillales;Streptococcaceae	0.01(0.02)	2.44(0.81)	0.01(0.02)	9.11(5.09)	0(0)	4.86(2.53)	0(0)	9.8(5.18)	n.s.	n.s.	1.6E-04	4.4E-04	0(0)	n.s.	4.4E-04	n.s.	n.s.		
			Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	8(6.17)	23.23(12.3)	3.83(4.19)	1.27(3.34)	4.71(3.19)	29.59(7.33)	1.69(5.31)	0(0.01)	n.s.	n.s.	2.4E-02	n.s.	1.4E-08	n.s.	8.0E-07	n.s.	n.s.		
			Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	1.34(0.84)	4.57(1.75)	0.25(0.33)	0.42(0.69)	1.37(0.67)	4.78(1.91)	0.06(0.02)	1.03(0.67)	n.s.	n.s.	3.0E-03	4.9E-03	7.2E-04	3.1E-02	2.1E-03	n.s.	1.3E-02		
			Firmicutes;Clostridia;Clostridiales;Incertae Sedis XIII	0.01(0.04)	0.1(0.16)	0.02(0.04)	0(0)	0.01(0.02)	0.18(0.12)	0(0)	0(0)	n.s.	n.s.	6.0E-03	n.s.	6.0E-03	n.s.	1.4E-02	n.s.	n.d.		
			Firmicutes;Clostridia;Clostridiales;Helicobacteraceae	0.21(0.2)	2.88(3.47)	0.57(0.76)	21.18(20.74)	1.74(1.3)	0.05(0.06)	0(0.01)	0.31(0.17)	n.s.	n.s.	1.9E-02	2.0E-02	n.s.	4.4E-02	n.s.	1.0E-03			
			Proteobacteria;Epsilonproteobacteria;Campylobacterales	5.07(3.58)	1.43(0.37)	1.58(1.59)	31.77(18.7)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	3.9E-02	n.d.	n.d.	n.d.	1.5E-02	5.3E-07	n.d.		
Genus			Actinobacteria;Actinobacteria;Coriobacteriaceae	0.01(0.02)	0.17(0.19)	0.05(0.06)	0.3(0.45)	0.15(0.09)	0.15(0.11)	0.01(0.02)	0.25(0.16)	n.s.	n.s.	6.8E-03	n.s.	n.s.	4.5E-02	n.s.	1.1E-02			
			Bacteroidetes;Bacteroides;Bacteroidaceae	0.62(0.18)	19.24(3.49)	8.95(13.02)	0(0)	5.23(1.92)	8.76(4.22)	2.76(8.73)	0(0)	n.s.	8.2E-04	n.s.	2.7E-04	1.6E-03	n.s.	8.6E-04				
			Bacteroidetes;Bacteroides;Parporhamnaceae;Parabacteroides	1.02(0.34)	0.77(0.37)	5.06(6.18)	0(0)	0.05(0.04)	0.28(0.23)	0(0)	0(0)	n.s.	n.s.	6.8E-03	n.s.	n.s.	8.8E-06	n.s.	n.s.			
			Bacteroidetes;Bacteroides;Prevotellaceae;Other	0.11(0.07)	0(0)	0.01(0.02)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	n.d.	n.d.	n.s.	1.2E-02	n.d.	n.d.				
			Bacteroidetes;Bacteroides;Prevotellaceae;Prevotella	2.94(1.18)	0.01(0.02)	0.56(0.88)	0(0)	0(0)	0(0)	0(0)	n.s.	n.s.	n.d.	n.d.	n.d.	1.5E-03	n.s.	5.1E-05				
			Bacteroidetes;Bacteroides;Rikenellaceae;Alistipes	1.14(0.72)	4.61(1.89)	0(0)	0(0)	0.73(0.37)	1.88(0.96)	0(0)	0(0)	n.s.	n.s.	1.8E-03	4.1E-04	5.3E-04	3.9E-02	n.s.	n.s.			
			Bacteroidetes;Bacteroides;Rikenellaceae;Other	9.78(6.87)	1.84(1.21)	5.59(12.66)	0(0)	17.24(7.68)	0.02(0.04)	1.44(3.81)	0(0.01)	n.s.	n.s.	9.2								